

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/590,705
Source: IFW0
Date Processed by STIC: 09/05/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 09/05/2006

PATENT APPLICATION: US/10/590,705

TIME: 15:10:31

Input Set : A:\5.1301 Sequence Listing.txt

Output Set: N:\CRF4\09052006\J590705.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
 5 <120> TITLE OF INVENTION: Method for producing amino acid
 7 <130> FILE REFERENCE: 1657
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/590,705
 C--> 9 <141> CURRENT FILING DATE: 2006-08-25
 9 <160> NUMBER OF SEQ ID NOS: 16
 10 <170> SOFTWARE: PatentIn Ver. 3.1
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 30
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Artificial
 17 <220> FEATURE:
 18 <223> OTHER INFORMATION: Synthetic DNA
 20 <400> SEQUENCE: 1
 21 ctgcttgccc tgcaggtgca ccagcaaacg 30
 23 <210> SEQ ID NO: 2
 24 <211> LENGTH: 30
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Synthetic DNA
 31 <400> SEQUENCE: 2
 32 cgagctgccc gacaaccagg aattcagcgg 30
 34 <210> SEQ ID NO: 3
 35 <211> LENGTH: 1404
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Corynebacterium glutamicum ATCC13032
 39 <220> FEATURE:
 40 <221> NAME/KEY: CDS
 W--> 41 <222> LOCATION:
 43 <400> SEQUENCE: 3
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 45 Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
 46 1 5 10 15
 48 gtc atc ggt tct ggt ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc 96
 49 Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
 50 20 25 30
 52 aag gca gac gtc gat gtc act ctg att gac cgc acc aac cac cac ctc 144
 53 Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
 54 35 40 45
 56 ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc tcc tcc ggt 192
 57 Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
 58 50 55 60

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60	gaa	atc	gca	cct	tcc	act	cga	cag	atc	ctg	ggc	tcc	cag	gaa	aac	gtc	240
61	Glu	Ile	Ala	Pro	Ser	Thr	Arg	Gln	Ile	Leu	Gly	Ser	Gln	Glu	Asn	Val	
62	65					70				75						80	
64	aac	gtc	atc	aag	ggc	gaa	gtc	acc	gac	atc	aac	gtc	gag	tcc	cag	act	288
65	Asn	Val	Ile	Lys	Gly	Glu	Val	Thr	Asp	Ile	Asn	Val	Glu	Ser	Gln	Thr	
66					85					90						95	
68	gtg	acc	gcc	tcc	ctg	ggc	gag	ttc	acc	cgc	gtt	ttt	gag	tac	gat	tcc	336
69	Val	Thr	Ala	Ser	Leu	Gly	Glu	Phe	Thr	Arg	Val	Phe	Glu	Tyr	Asp	Ser	
70				100						105						110	
72	ttg	gtc	gtt	ggt	gct	ggc	gca	ggt	cag	tcc	tac	ttc	ggc	aat	gat	cac	384
73	Leu	Val	Val	Gly	Ala	Gly	Ala	Gly	Gln	Ser	Tyr	Phe	Gly	Asn	Asp	His	
74				115						120						125	
76	ttc	gct	gag	ttc	gca	cct	ggc	atg	aag	tcc	atc	gac	gat	gca	ctg	gag	432
77	Phe	Ala	Glu	Phe	Ala	Pro	Gly	Met	Lys	Ser	Ile	Asp	Asp	Ala	Leu	Glu	
78				130						135						140	
80	att	cgt	gca	cgc	atc	atc	ggt	gct	ttc	gag	cgc	gct	gag	atc	tgc	gag	480
81	Ile	Arg	Ala	Arg	Ile	Ile	Gly	Ala	Phe	Glu	Arg	Ala	Glu	Ile	Cys	Glu	
82	145					150										160	
84	gat	cca	gct	gag	cgc	gaa	cgc	ctg	ctc	acc	ttc	gtc	gtt	gtt	ggc	gct	528
85	Asp	Pro	Ala	Glu	Arg	Glu	Arg	Leu	Leu	Thr	Phe	Val	Val	Val	Gly	Ala	
86						165										175	
88	ggc	cca	acc	ggt	gtt	gag	ctt	gct	ggc	cag	ttg	gct	gag	atg	gct	cac	576
89	Gly	Pro	Thr	Gly	Val	Glu	Leu	Ala	Gly	Gln	Leu	Ala	Glu	Met	Ala	His	
90						180										190	
92	cgc	acc	ctt	gct	ggt	gag	tac	aag	aac	ttc	aac	acc	aac	tcc	gca	aag	624
93	Arg	Thr	Leu	Ala	Gly	Glu	Tyr	Lys	Asn	Phe	Asn	Thr	Asn	Ser	Ala	Lys	
94						195										205	
96	atc	atc	ctg	ctt	gat	ggt	gct	cca	cag	gtt	ctt	cct	cca	ttc	ggt	aag	672
97	Ile	Ile	Leu	Leu	Asp	Gly	Ala	Pro	Gln	Val	Leu	Pro	Pro	Phe	Gly	Lys	
98						210										220	
100	cgc	cta	ggc	cgc	aac	gca	cag	cgc	acc	ctg	gaa	aag	atg	ggt	gtc	aac	720
101	Arg	Leu	Gly	Arg	Asn	Ala	Gln	Arg	Thr	Leu	Glu	Lys	Met	Gly	Val	Asn	
102	225					230										240	
104	gtt	cgc	ctg	aac	gct	atg	gtc	acc	aac	gtt	gac	gct	acc	tcg	gtc	acc	768
105	Val	Arg	Leu	Asn	Ala	Met	Val	Thr	Asn	Val	Asp	Ala	Thr	Ser	Val	Thr	
106						245										255	
108	tac	aag	acc	aag	gac	ggc	gaa	gag	cac	acc	atc	gaa	tct	ttc	tgc	aag	816
109	Tyr	Lys	Thr	Lys	Asp	Gly	Glu	Glu	His	Thr	Ile	Glu	Ser	Phe	Cys	Lys	
110						260										270	
112	att	tgg	tcc	gct	ggt	gtt	gcg	gca	tcc	cca	ctg	ggc	aag	ctc	gtc	gca	864
113	Ile	Trp	Ser	Ala	Gly	Val	Ala	Ala	Ser	Pro	Leu	Gly	Lys	Leu	Val	Ala	
114						275										285	
116	gag	cag	acc	ggt	gtt	gag	acc	gac	cgc	gca	ggc	cgc	gtc	atg	gtt	aac	912
117	Glu	Gln	Thr	Gly	Val	Glu	Thr	Asp	Arg	Ala	Gly	Arg	Val	Met	Val	Asn	
118						290										300	
120	gat	gac	ctg	tct	gtt	ggc	gat	cag	aag	aac	gtc	ttc	gtt	gtt	ggc	gac	960
121	Asp	Asp	Leu	Ser	Val	Gly	Asp	Gln	Lys	Asn	Val	Phe	Val	Val	Gly	Asp	
122	305					310										320	
124	atg	atg	aac	tac	aac	aac	ctc	cct	ggt	gtt	gct	cag	gta	gca	atc	cag	1008

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125 Met Met Asn Tyr Asn Asn Leu Pro Gly Val Ala Gln Val Ala Ile Gln
126                               325                               330                               335
128 agt ggt gag tac gtt gct gag cag atc gaa gct gag gtt gaa ggc cgc 1056
129 Ser Gly Glu Tyr Val Ala Glu Gln Ile Glu Ala Glu Val Glu Gly Arg
130                               340                               345                               350
132 tcc aac acc gag cgc gaa gct ttc gat tac ttc gac aag ggc tcc atg 1104
133 Ser Asn Thr Glu Arg Glu Ala Phe Asp Tyr Phe Asp Lys Gly Ser Met
134                               355                               360                               365
136 gct acc att tcc cgc ttc tcc gca gtg gtg aag atg ggc aag gtt gag 1152
137 Ala Thr Ile Ser Arg Phe Ser Ala Val Val Lys Met Gly Lys Val Glu
138                               370                               375                               380
140 gtc acc ggc ttc atc ggt tgg gtt ctg tgg ttg gct gtt cac atc atg 1200
141 Val Thr Gly Phe Ile Gly Trp Val Leu Trp Leu Ala Val His Ile Met
142 385                               390                               395                               400
144 ttc ctg gtt ggc ttc cgc aac cgt ttc gtc tcc gca atc agc tgg ggc 1248
145 Phe Leu Val Gly Phe Arg Asn Arg Phe Val Ser Ala Ile Ser Trp Gly
146                               405                               410                               415
148 ctg aac gca ctg tcc cgc aag cgt tgg aac ctg gca acc acc cgc cag 1296
149 Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln
150                               420                               425                               430
152 cag ctc cac tca cgc acc acg ctg tcc aag ttc gct cac gag ctt gag 1344
153 Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu
154                               435                               440                               445
156 gaa gca tct tct gat ctt cca atc gag ctg cgc gac aac cag cgt ttc 1392
157 Glu Ala Ser Ser Asp Leu Pro Ile Glu Leu Arg Asp Asn Gln Arg Phe
158 450                               455                               460
160 agc gga aag taa 1404
161 Ser Gly Lys
162 465
164 <210> SEQ ID NO: 4
165 <211> LENGTH: 467
166 <212> TYPE: PRT
167 <213> ORGANISM: Corynebacterium glutamicum ATCC13032
169 <400> SEQUENCE: 4
170 Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
171 1 5 10 15
173 Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
174 20 25 30
176 Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
177 35 40 45
179 Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
180 50 55 60
183 Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
184 65 70 75 80
186 Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
187 85 90 95
189 Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
190 100 105 110
192 Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His

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193          115          120          125
195 Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
196          130          135          140
198 Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
199 145          150          155          160
201 Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
202          165          170          175
204 Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
205          180          185          190
207 Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
208          195          200          205
210 Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
211          210          215          220
213 Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
214 225          230          235          240
216 Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
217          245          250          255
219 Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
220          260          265          270
222 Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
223          275          280          285
225 Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
226          290          295          300
228 Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val Val Gly Asp
229 305          310          315          320
231 Met Met Asn Tyr Asn Asn Leu Pro Gly Val Ala Gln Val Ala Ile Gln
232          325          330          335
234 Ser Gly Glu Tyr Val Ala Glu Gln Ile Glu Ala Glu Val Glu Gly Arg
235          340          345          350
237 Ser Asn Thr Glu Arg Glu Ala Phe Asp Tyr Phe Asp Lys Gly Ser Met
238          355          360          365
240 Ala Thr Ile Ser Arg Phe Ser Ala Val Val Lys Met Gly Lys Val Glu
241          370          375          380
243 Val Thr Gly Phe Ile Gly Trp Val Leu Trp Leu Ala Val His Ile Met
244 385          390          395          400
246 Phe Leu Val Gly Phe Arg Asn Arg Phe Val Ser Ala Ile Ser Trp Gly
247          405          410          415
249 Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln
250          420          425          430
252 Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu
253          435          440          445
255 Glu Ala Ser Ser Asp Leu Pro Ile Glu Leu Arg Asp Asn Gln Arg Phe
256          450          455          460
258 Ser Gly Lys
259 465
261 <210> SEQ ID NO: 5
263 <211> LENGTH: 1362
264 <212> TYPE: DNA
265 <213> ORGANISM: Corynebacterium diphtheriae

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267 <220> FEATURE:
 268 <221> NAME/KEY: CDS
 W--> 269 <222> LOCATION:
 271 <400> SEQUENCE: 5

272	atg	act	aac	acc	cca	ttt	cgc	cca	gaa	ggt	gga	cgc	cac	cac	gtt	gta	48
273	Met	Thr	Asn	Thr	Pro	Phe	Arg	Pro	Glu	Gly	Gly	Arg	His	His	Val	Val	
274	1				5				10						15		
276	gtt	att	ggc	tcc	ggc	ttc	ggt	gga	cta	ttc	gca	gtt	caa	aac	ctc	aaa	96
277	Val	Ile	Gly	Ser	Gly	Phe	Gly	Gly	Leu	Phe	Ala	Val	Gln	Asn	Leu	Lys	
278				20					25					30			
280	gat	gca	gat	gtc	gat	atc	acc	ctc	atc	gac	cgg	aca	aac	cac	cac	ctt	144
281	Asp	Ala	Asp	Val	Asp	Ile	Thr	Leu	Ile	Asp	Arg	Thr	Asn	His	His	Leu	
282				35					40					45			
284	ttc	cag	ccg	ttg	ctt	tac	caa	gta	gca	acc	ggt	atc	ttg	tcg	tct	ggt	192
285	Phe	Gln	Pro	Leu	Leu	Tyr	Gln	Val	Ala	Thr	Gly	Ile	Leu	Ser	Ser	Gly	
286		50					55					60					
288	gaa	atc	gca	cca	caa	acg	cgt	caa	gtt	ctt	gca	cag	caa	aat	aat	gtg	240
289	Glu	Ile	Ala	Pro	Gln	Thr	Arg	Gln	Val	Leu	Ala	Gln	Gln	Asn	Asn	Val	
290	65					70			75							80	
292	cac	gtt	ctt	aag	gct	gaa	gtc	acc	gac	att	gac	acc	gaa	tcg	aag	acg	288
293	His	Val	Leu	Lys	Ala	Glu	Val	Thr	Asp	Ile	Asp	Thr	Glu	Ser	Lys	Thr	
294				85					90						95		
296	gtc	gtc	gca	gac	ttg	gat	gat	tat	tct	aaa	aca	att	gaa	tac	gat	tcc	336
297	Val	Val	Ala	Asp	Leu	Asp	Asp	Tyr	Ser	Lys	Thr	Ile	Glu	Tyr	Asp	Ser	
298				100					105					110			
300	ctg	atc	gtc	gcc	gct	ggt	gca	ggt	cag	tct	tac	ttc	gga	aat	gat	cac	384
301	Leu	Ile	Val	Ala	Ala	Gly	Ala	Gly	Gln	Ser	Tyr	Phe	Gly	Asn	Asp	His	
302			115					120					125				
304	ttc	gcg	gaa	ttc	gcg	ccg	ggt	atg	aaa	aca	atc	gat	gat	gca	ctc	gaa	432
305	Phe	Ala	Glu	Phe	Ala	Pro	Gly	Met	Lys	Thr	Ile	Asp	Asp	Ala	Leu	Glu	
306		130					135					140					
308	ctg	cgt	gcg	cgc	atc	atc	ggc	gct	ttc	gaa	cgc	gca	gaa	atg	tgc	gaa	480
309	Leu	Arg	Ala	Arg	Ile	Ile	Gly	Ala	Phe	Glu	Arg	Ala	Glu	Met	Cys	Glu	
310	145					150				155					160		
312	gat	ccc	aaa	gaa	cgt	gaa	cgc	ctc	ttg	act	ttt	gtt	atc	gtt	ggc	gca	528
313	Asp	Pro	Lys	Glu	Arg	Glu	Arg	Leu	Leu	Thr	Phe	Val	Ile	Val	Gly	Ala	
314				165					170						175		
317	gga	cca	aca	ggc	gta	gaa	ctt	gca	ggt	cag	ctg	gcc	gaa	atg	gca	cac	576
318	Gly	Pro	Thr	Gly	Val	Glu	Leu	Ala	Gly	Gln	Leu	Ala	Glu	Met	Ala	His	
319				180					185					190			
321	cgc	acg	ttg	tct	gga	gag	tac	acg	cag	ttc	acg	cct	tcc	aac	gcg	aag	624
322	Arg	Thr	Leu	Ser	Gly	Glu	Tyr	Thr	Gln	Phe	Thr	Pro	Ser	Asn	Ala	Lys	
323			195					200					205				
325	atc	atc	ctg	ctt	gac	ggc	gct	cct	cag	gtg	ctt	cca	ccg	ttc	ggc	aag	672
326	Ile	Ile	Leu	Leu	Asp	Gly	Ala	Pro	Gln	Val	Leu	Pro	Pro	Phe	Gly	Lys	
327		210					215					220					
329	cgt	ttg	ggt	cgt	act	gca	cag	cgt	gaa	tta	gaa	aag	att	ggt	gta	acg	720
330	Arg	Leu	Gly	Arg	Thr	Ala	Gln	Arg	Glu	Leu	Glu	Lys	Ile	Gly	Val	Thr	
331	225					230					235					240	

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2

VERIFICATION SUMMARY

DATE: 09/05/2006

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:41 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:3, CDS LOCATION:
L:269 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:5, CDS LOCATION:
L:490 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION:
L:701 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:9, CDS LOCATION:
L:906 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION:
L:1113 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:13, CDS LOCATION:
L:1326 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:15, CDS LOCATION: